

Query= SEQ ID NO:1  
(1509 letters)

Sequences producing significant alignments:	Score (bits)	E Value
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Contig:AC119673.2.1.188119	<u>460</u>	e-126
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>Contig:AC119673.2.1.188119  
Length = 188119

Score = 460 bits (232), Expect = e-126  
Identities = 235/236 (99%)  
Strand = Plus / Minus

Query: 255	agtctttcctacagtggtcagcaccagctttatccagcatgaagtcgtggaagagtatag	314
Sbjct: 172797	agtctttcctacagtggtcagcaccagctttatccagcatgaagtcgtggaagagtatag	172738

Query: 315	ccacctgttcactatccaaggctcggaccccagcttgcagccctacctgctgatggctca	374
Sbjct: 172737	ccacctgttcactatccaaggctcggaccccagcttgcagccctacctgctgatggctca	172678

Query: 375	ctttgatgtggtgcctgcccctgaagaaggctgggaggtgccccattctctgggttga	434
Sbjct: 172677	ctttgatgtggtgcctgcccctgaagaaggctgggaggtgccccattctctgggttga	172618

Query: 435	gcgtgatggcgatcatctatggtcggggcacactggacgacaagaactctgtgatgg	490
Sbjct: 172617	gcgtgatggcgatcatctatggtcggggcacactggacgacaagaactctgtgatgg	172562

Score = 341 bits (172), Expect = 8e-91  
Identities = 172/172 (100%)  
Strand = Plus / Minus

Query: 1114	gaggtcctagaactcacgaagaacattgtggctgataacagagtccagttccatgtgtg	1173
Sbjct: 160007	gaggtcctagaactcacgaagaacattgtggctgataacagagtccagttccatgtgtg	159948

Query: 1174	agtgcctttgacccccctccccgtcagcccttctgatgacaaggccttgggctaccagctg	1233
Sbjct: 159947	agtgcctttgacccccctccccgtcagcccttctgatgacaaggccttgggctaccagctg	159888

Query: 1234	ctccgccagaccgtacagtccgtcttcccgaagtcaatattactgccccag	1285
Sbjct: 159887	ctccgccagaccgtacagtccgtcttcccgaagtcaatattactgccccag	159836

Score = 341 bits (172), Expect = 8e-91  
Identities = 172/172 (100%)  
Strand = Plus / Minus

Query: 1 atggctcagcgggtgcgtttgcgtgctggccctgggtggctatgctgctcctagttttccct 60  
|||||  
Sbjct: 177310 atggctcagcgggtgcgtttgcgtgctggccctgggtggctatgctgctcctagttttccct 177251

Query: 61 accgtctccagatcgatgggcccaggagcggggagcatcaaagggcgctcgcaatccct 120  
|||||  
Sbjct: 177250 accgtctccagatcgatgggcccaggagcggggagcatcaaagggcgctcgcaatccct 177191

Query: 121 tctcagttcagcaaagaggaacgcgtcgcgatgaaagaggcgctgaaagggtg 172  
|||||  
Sbjct: 177190 tctcagttcagcaaagaggaacgcgtcgcgatgaaagaggcgctgaaagggtg 177139

Score = 266 bits (134), Expect = 4e-68  
Identities = 134/134 (100%)  
Strand = Plus / Minus

Query: 575 agtcatcagggacaggggctcagaggatctcagccctgctacagtcaaggggcgtccagc 634  
|||||  
Sbjct: 171457 agtcatcagggacaggggctcagaggatctcagccctgctacagtcaaggggcgtccagc 171398

Query: 635 tagccttcattgtggacgaggggggcttcattcttgatgatttcattcctaacttcaaga 694  
|||||  
Sbjct: 171397 tagccttcattgtggacgaggggggcttcattcttgatgatttcattcctaacttcaaga 171338

Query: 695 agcccatcgcccttg 708  
|||||  
Sbjct: 171337 agcccatcgcccttg 171324

Score = 248 bits (125), Expect = 9e-63  
Identities = 125/125 (100%)  
Strand = Plus / Minus

Query: 1385 gcatccatggagtcaacgagaaaaatctcagtccaagcctatgagaccaagtgaattca 1444  
|||||  
Sbjct: 155447 gcatccatggagtcaacgagaaaaatctcagtccaagcctatgagaccaagtgaattca 155388

Query: 1445 tctttgagttgattcagaatgctgacacagaccaggagccagtttctcacctgcacaaac 1504  
|||||  
Sbjct: 155387 tctttgagttgattcagaatgctgacacagaccaggagccagtttctcacctgcacaaac 155328

Query: 1505 tgtga 1509  
|||||  
Sbjct: 155327 tgtga 155323

Score = 238 bits (120), Expect = 8e-60  
Identities = 120/120 (100%)  
Strand = Plus / Minus

Query: 708 gattgcagtctcagagaaggggtccatgaacctcatgctgcaagtaaacaatgacttcagg 767  
|||||  
Sbjct: 171024 gattgcagtctcagagaaggggtccatgaacctcatgctgcaagtaaacaatgacttcagg 170965

Query: 768 ccactcttcagctcctccaaaggagacaagcattggcatccttgcaagctgctgtcagccg 827  
|||||  
Sbjct: 170964 ccactcttcagctcctccaaaggagacaagcattggcatccttgcaagctgctgtcagccg 170905

Score = 202 bits (102), Expect = 5e-49  
Identities = 102/102 (100%)  
Strand = Plus / Minus

Query: 1284 agttacttctattggcaacacagacagccgattctttacaaacctcaccactggcatcta 1343  
|||||  
Sbjct: 157084 agttacttctattggcaacacagacagccgattctttacaaacctcaccactggcatcta 157025

Query: 1344 caggttctacccccatctacatacagcctgaagacttcaaacg 1385  
|||||  
Sbjct: 157024 caggttctacccccatctacatacagcctgaagacttcaaacg 156983

Score = 178 bits (90), Expect = 7e-42  
Identities = 93/94 (98%)  
Strand = Plus / Minus

Query: 163 ctgaaagggtgcatccagattccaacagtgacttttagctctgagaagtccaataactaca 222  
|||||  
Sbjct: 175216 ctgacagggtgcatccagattccaacagtgacttttagctctgagaagtccaataactaca 175157

Query: 223 gccctggctgagttcggaataacattcataaag 256  
|||||  
Sbjct: 175156 gccctggctgagttcggaataacattcataaag 175123

Score = 174 bits (88), Expect = 1e-40  
Identities = 88/88 (100%)  
Strand = Plus / Minus

Query: 489 ggcattactgcaggccttggagctcctgctgatcaggaagtacatccccgaagatcttt 548  
|||||  
Sbjct: 172136 ggcattactgcaggccttggagctcctgctgatcaggaagtacatccccgaagatcttt 172077

Query: 549 cttcatttctctgggccatgatgaggag 576  
|||||  
Sbjct: 172076 cttcatttctctgggccatgatgaggag 172049

Score = 161 bits (81), Expect = 2e-36  
Identities = 81/81 (100%)  
Strand = Plus / Minus

Query: 964 aggtttatggagagaaatcccttaaccaatgcaataatcaggaccaccacggcactcacc 1023  
|||||  
Sbjct: 169129 aggtttatggagagaaatcccttaaccaatgcaataatcaggaccaccacggcactcacc 169070

Query: 1024 atattcaaagcaggggtcaag 1044  
|||||  
Sbjct: 169069 atattcaaagcaggggtcaag 169049

Score = 153 bits (77), Expect = 4e-34  
Identities = 77/77 (100%)  
Strand = Plus / Minus

Query: 827 gattggagcagacaccaatgcctatcatatttgggaagcgggacagtgggtgactgtattgc 886  
|||||  
Sbjct: 169990 gattggagcagacaccaatgcctatcatatttgggaagcgggacagtgggtgactgtattgc 169931

Query: 887 agcaactggcaaatgag 903  
|||||  
Sbjct: 169930 agcaactggcaaatgag 169914

Score = 151 bits (76), Expect = 2e-33  
Identities = 76/76 (100%)  
Strand = Plus / Minus

Query: 1043 agttcaatgtcatccccccagtggcccaggccacagtcaacttccggattcaccctggac 1102  
|||||  
Sbjct: 167563 agttcaatgtcatccccccagtggcccaggccacagtcaacttccggattcaccctggac 167504

Query: 1103 agacagtccaagaggt 1118  
|||||||  
Sbjct: 167503 agacagtccaagaggt 167488

Score = 131 bits (66), Expect = 1e-27  
Identities = 66/66 (100%)  
Strand = Plus / Minus

Query: 902 agtttcccttccctgtcaatataatcctgagcaacccatggctatttgaaccacttataa 961  
|||||||  
Sbjct: 169455 agtttcccttccctgtcaatataatcctgagcaacccatggctatttgaaccacttataa 169396

Query: 962 gcaggt 967  
|||||  
Sbjct: 169395 gcaggt 169390

Query= SEQ ID NO:3  
(1086 letters)

Sequences producing significant alignments:	Score (bits)	E Value
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Contig:AC119673.2.1.188119	<u>460</u>	e-127
----------------------------	------------	-------

>Contig:AC119673.2.1.188119  
Length = 188119

Score = 460 bits (232), Expect = e-127  
Identities = 235/236 (99%)  
Strand = Plus / Minus

Query: 255	agtctttcctacagtggtcagcaccagctttatccagcatgaagtcgctggaagagtatag	314
Sbjct: 172797	agtctttcctacagtggtcagcaccagctttatccagcatgaagtcgctggaagagtatag	172738

Query: 315	ccacctgttcactatccaaggctcggaccccagcttgcagccctacctgctgatggctca	374
Sbjct: 172737	ccacctgttcactatccaaggctcggaccccagcttgcagccctacctgctgatggctca	172678

Query: 375	ctttgatgtggtgcctgccccctgaagaaggctgggaggtgccccattctctgggttgga	434
Sbjct: 172677	ctttgatgtggtgcctgccccctgaagaaggctgggaggtgccccattctctgggttgga	172618

Query: 435	gcgtgatggcgatcatctatggctcggggcacactggacgacaagaactctgtgatgg	490
Sbjct: 172617	gcgtgatggcgatcatctatggctcggggcacactggacgacaagaactctgtgatgg	172562

Score = 341 bits (172), Expect = 6e-91  
Identities = 172/172 (100%)  
Strand = Plus / Minus

Query: 1	atggctcagcgggtgcgtttgcgtgctggccctgggtggctatgctgctcctagttttccct	60
Sbjct: 177310	atggctcagcgggtgcgtttgcgtgctggccctgggtggctatgctgctcctagttttccct	177251

Query: 61	accgtctccagatcgatgggccccgaggagcggggagcatcaaagggcgctcggaatccct	120
Sbjct: 177250	accgtctccagatcgatgggccccgaggagcggggagcatcaaagggcgctcggaatccct	177191

Query: 121	tctcagttcagcaaagaggaacgcgtcgcatgaaagaggcgctgaaagggtg	172
Sbjct: 177190	tctcagttcagcaaagaggaacgcgtcgcatgaaagaggcgctgaaagggtg	177139

Score = 266 bits (134), Expect = 3e-68  
Identities = 134/134 (100%)  
Strand = Plus / Minus

Query: 575 agtcatcagggacaggggctcagaggatctcagccctgctacagtcaaggggcgtccagc 634  
|||||  
Sbjct: 171457 agtcatcagggacaggggctcagaggatctcagccctgctacagtcaaggggcgtccagc 171398

Query: 635 tagccttcattgtggacgaggggggcttcattcttgatgatttcattcctaacttcaaga 694  
|||||  
Sbjct: 171397 tagccttcattgtggacgaggggggcttcattcttgatgatttcattcctaacttcaaga 171338

Query: 695 agcccatcgcccttg 708  
|||||  
Sbjct: 171337 agcccatcgcccttg 171324

Score = 238 bits (120), Expect = 6e-60  
Identities = 120/120 (100%)  
Strand = Plus / Minus

Query: 708 gattgcagtctcagagaaggggtccatgaacctcatgctgcaagtaaacaatgacttcagg 767  
|||||  
Sbjct: 171024 gattgcagtctcagagaaggggtccatgaacctcatgctgcaagtaaacaatgacttcagg 170965

Query: 768 ccactcttcagctcctccaaaggagacaagcattggcatccttgagctgctgtcagccg 827  
|||||  
Sbjct: 170964 ccactcttcagctcctccaaaggagacaagcattggcatccttgagctgctgtcagccg 170905

Score = 178 bits (90), Expect = 5e-42  
Identities = 93/94 (98%)  
Strand = Plus / Minus

Query: 163 ctgaaagggtgcatccagattccaacagtgacttttagctctgagaagtccaataactaca 222  
|||||  
Sbjct: 175216 ctgacagggtgcatccagattccaacagtgacttttagctctgagaagtccaataactaca 175157

Query: 223 gccctggctgagttcggaataacattcataaag 256  
|||||  
Sbjct: 175156 gccctggctgagttcggaataacattcataaag 175123

Score = 174 bits (88), Expect = 7e-41  
Identities = 88/88 (100%)  
Strand = Plus / Minus

Query: 489 ggcattactgcaggccttggagctcctgctgatcaggaagtacatccccgaagatcttt 548  
|||||  
Sbjct: 172136 ggcattactgcaggccttggagctcctgctgatcaggaagtacatccccgaagatcttt 172077

Query: 549 cttcatttctctgggccatgatgaggag 576  
|||||  
Sbjct: 172076 cttcatttctctgggccatgatgaggag 172049

Score = 161 bits (81), Expect = 1e-36  
Identities = 81/81 (100%)  
Strand = Plus / Minus

Query: 902 aggtttatggagagaaatcccttaaccaatgcaataatcaggaccaccacggcactcacc 961  
|||||  
Sbjct: 169129 aggtttatggagagaaatcccttaaccaatgcaataatcaggaccaccacggcactcacc 169070

Query: 962 atattcaaagcaggggtcaag 982  
|||||  
Sbjct: 169069 atattcaaagcaggggtcaag 169049

Score = 157 bits (79), Expect = 2e-35  
Identities = 79/79 (100%)  
Strand = Plus / Minus

Query: 827 gattggagcagacaccaatgcctatcatatttggaagcgggacagtgggtgactgtattgc 886  
|||||  
Sbjct: 169990 gattggagcagacaccaatgcctatcatatttggaagcgggacagtgggtgactgtattgc 169931

Query: 887 agcaactggcaaagaggt 905  
|||||  
Sbjct: 169930 agcaactggcaaagaggt 169912

Score = 151 bits (76), Expect = 1e-33  
Identities = 76/76 (100%)  
Strand = Plus / Minus

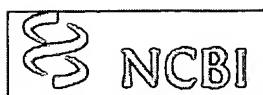
Query: 981 agttcaatgtcatccccccagtggcccaggccacagtcaacttccggattcaccctggac 1040  
|||||  
Sbjct: 167563 agttcaatgtcatccccccagtggcccaggccacagtcaacttccggattcaccctggac 167504



Query: 1041 agacagtccaagaggt 1056  
          |||||  
Sbjct: 167503 agacagtccaagaggt 167488

Score = 69.9 bits (35), Expect = 3e-09  
Identities = 35/35 (100%)  
Strand = Plus / Minus

Query: 1052 gaggtcctagaactcacgaagaacattgtggctga 1086  
          |||||  
Sbjct: 160007 gaggtcctagaactcacgaagaacattgtggctga 159973



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File

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Featur

☐ 1: AC119673. Homo sapiens chro...[gi:34610310]

Links

LOCUS AC119673 187660 bp DNA linear PRI 13-SEP-2003  
 DEFINITION Homo sapiens chromosome 1 clone RP11-212H11, complete sequence.  
 ACCESSION AC119673 AL365208  
 VERSION AC119673.3 GI:34610310  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 187660)  
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
 Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and  
 Haugen,E.D.  
 TITLE Direct Submission  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 187660)  
 AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-APR-2002) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 REFERENCE 3 (bases 1 to 187660)  
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
 Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.  
 and Haugen,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUL-2002) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 REFERENCE 4 (bases 1 to 187660)  
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
 Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and  
 Haugen,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-SEP-2003) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 COMMENT On Sep 13, 2003 this sequence version replaced gi:21844627.  
 ----- Genome Center  
 Center: University of Washington Genome Center  
 Center Code: UWGC  
 Web site: <http://www.genome.washington.edu>  
 Contact: uwgchtgs@u.washington.edu  
 Drafting Center: SC  
 ----- Project Information  
 Center project name: chr-1  
 Center clone name: RP11-212H11 (sc0653)  
 ----- Summary Statistics  
 Sequencing vector: unknown; 5% of reads  
 Sequencing vector: plasmid; 95% of reads  
 Chemistry: Dye-terminator ET; 43% of reads